Amendments to the Specification

Please replace the paragraph beginning on page 7, line 34 and ending on page 8, line 18 with the following replacement paragraph.

As used herein, "PDZ domain" refers to a protein module capable of binding to a target protein by recognition of the target's C-terminal or N-terminal amino acid sequence. PDZ domains are typically 85-95 amino acids in length and are found naturally in a variety of organisms ranging from bacteria to humans. An example PDZ domain is the PDZ domain of hCASK having the sequence SEQ ID NO: 2. A further example PDZ domain is the third PDZ domain of human Dlg1, such as shown within SEQ ID NO:9 (see Example 16). Other PDZ domains, according to the invention, have homology to the PDZ domain of SEQ ID NO: 2 or SEQ ID NO: 9, such as at least about 50 % identity using BLAST (default parameters). The name PDZ is derived from: PSD-95 (Cho et al., Neuron 9:929-942, 1992), Dlg-A (Woods and Bryant, Cell 66:451-464, 1991) and ZO-1 (Itoh et al., J. Cell. Biol. 121:491-502, 1993), each of which contains three such domains. PDZ domains have also been called GLGF repeats or DHRs and are identified in a variety of proteins (Ponting and Phillips, Trends Biochem. Sci. 20:102-103, 1995). A PDZ domain of PTPL1 has been shown to interact with the C-terminal tail of the membrane receptor Fas (Sato et al., 1995) and PDZ domains of PSD-95 bind to the C-terminals of the NMDA-receptor and Shaker-type K^+channels (Kim et al., Nature 378:85-88, 1995; Kornau et al., Science 269:1737-1740, 1995). The crystal structures of different PDZ domains have been published (e.g., Doyle et al., Cell .85:1067-1076, 1996; Morais Cabral et al., Nature 382:649-652, 1996). The PDZ domain of human CASK/LIN-2, also called hCASK, is well studied: its substrate specificity has been investigated (Cohen et al., 1998, J Cell Biol, 142: 129-38.) and its crystal structure determined (Daniels et al., 1998, Nat Struct Biol, 5: 317-25.). One skilled in the art can readily recognize and identify a PDZ domain, for example, by using the CD-Search computer program available at ~~www.ncbi.nlm.gov/Structure/cdd/cdd.shtml~~ the National Center for Biotechnology Information (NCBI) website, the NIH's free "Conserved Domain Database and Search Service".

Please replace the paragraph beginning on page 9, line 26 and ending on page 10, line 5 with the following replacement paragraph.

As used herein, the term "variant" is meant to indicate a polypeptide differing from another polypeptide by one or more amino acid substitutions resulting from engineered mutations in the gene coding for the polypeptide. One skilled in the art can readily recognize and identify a variant of a PDZ domain, for

example, by using the CD-Search computer program available at ~~www.ncbi.nlm.gov/Structure/cdd/cdd.shtml~~ the National Center for Biotechnology Information (NCBI) website, the NIH's free "Conserved Domain Database and Search Service" which can identify protein domains such as the PDZ domain and its variants. A polypeptide is typically no longer considered a variant of a parent polypeptide when the degree of homology between these polypeptides falls below about 40%, as ascertained for example by using the program BLAST to align two sequences (default parameters) described by Tatiana A. Tatusova and Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250. In some embodiments, variants have at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 97%, at least about 98%, at least about 99% homology with the parent polypeptide, as ascertained for example by using the program BLAST to align two sequences (default parameters). In some embodiments, a parent polypeptide can be evolved *in vitro* using directed evolution to yield one or more variants of the parent polypeptide. These variants can have new or improved properties compared to the parent polypeptide or be useful in generating further variants.